

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 22, 2005, 23:34:02 ; Search time 2378.54 Seconds
(without alignments)
4701.242 Million cell updates/sec

Title: US-10-614-282-1

Perfect score: 239

Sequence: 1 atcagtcacgacttggttaag.....tctggttcggcgtgacaat 239

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	239	100.0	510	3	BI375946
2	145.4	60.8	379	7	CO306026
3	37.2	15.6	1138	3	BQ144508
4	35.6	14.9	162	5	BW068571
5	35.2	14.7	625	10	CL579846
6	35.2	14.7	712	10	CL574949
7	35	14.6	496	2	BF024030
8	34.8	14.6	625	6	CD648340
9	34.6	14.5	563	9	A2581975
10	34.4	14.4	698	8	DN983220
11	34	14.2	670	11	LBFA025H06
12	34	14.2	670	11	LBFA025H09
13	33.8	14.1	507	10	EX137891
14	33.6	14.1	638	9	A2983355
15	33.6	14.1	833	10	CZ712792
16	33.4	14.0	845	6	CF813122
17	33.4	14.0	849	7	CO014533
18	33.4	14.0	855	6	CF818084
19	33.4	14.0	1026	4	AF227817
20	33.2	13.9	537	5	BQ743358
21	33.2	13.9	557	3	BJ645949
22	33	13.8	273	10	CZ915578
					CZ915578 4013012B0

23	32.8	13.7	349	5	BU578178
24	32.8	13.7	438	1	AW133037
25	32.8	13.7	443	2	BE803253
26	32.8	13.7	446	2	BG725287
27	32.8	13.7	642	7	CV504660
28	32.8	13.7	773	9	BA465834
29	32.8	13.7	955	5	BU901940
c	30	32.6	624	10	EX139003
	31	32.6	827	7	CO035667
	32	32.6	852	6	CD649081
	33	32.6	866	7	CO031945
	34	32.6	895	6	CD048532
	35	32.4	607	10	CW060437
	36	32.4	616	7	CK571307
	37	32.4	680	10	CW463755
c	38	32.4	691	10	CW229198
c	39	32.4	835	10	CW987242
	40	32.2	483	7	CN242214
c	41	32.2	565	5	BY492451
c	42	32.2	648	10	CE691717
c	43	32.2	664	2	BE941338
	44	32	134	1	AU077131
c	45	32	457	1	AJ791110

ALIGNMENTS

RESULT 1
BI375946
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

BI375946 510 bp mRNA linear EST 16-JAN-2004
RE63854.5prime RE Drosophila melanogaster normalized Embryo pFlc-1
Drosophila melanogaster cDNA clone RE63854 5, mRNA sequence.

BI375946
GI:15071974
EST.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 510)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,
Carlson, J., Chavez, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G.,
Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and
Rubin, G.M.
BDGP/HMI RE Drosophila EST Project
Unpublished (2001)
Other ESTs: RE63854.3prime
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
hit genomic AB003674: arm:3R [2306679,2604706]
estimated-cyto:83FI-84A5: 05/16/2001
Plate: RE.638 row: E column: 6
High quality sequence stop: 453.
Location/Qualifiers
1..510
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="RE63854"
/sex="male and female"
/dev_stage="0-24 hours mixed stage embryonic"
/lab_hosts="DHS-alpha Tona"
/clone_lib="RE Drosophila melanogaster normalized Embryo
pFlc-1"
/note="Organ: embryo; Vector: pFlc1; Site_1: XhoI; Site_2: